March 12, 2002

Via DHL

U.S. Patent and Trademark Office
Crystal Mall I
Seventh Floor, Receptionist
Attn: Examiner William Moore, Art Unit 1652
1911 South Clark Street
Arlington, VA 22202

Re: U.S. Application No. 09/652,743 filed August 31, 2000
      "Proteases and Variants Thereof"

Dear Examiner Moore:

As per your request, enclosed is a computer readable form of the Sequence Listing mailed on October 22, 2001. The content of the paper copy that was filed on October 22, 2001 and of the enclosed computer readable form is the same. This submission contains no new matter.

If you have any questions, please do not hesitate to contact me.

Very truly yours,

Elias J. Lambiris
Director, Patents – US

Wi Moore

/600 RUSH

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/652,743A

ENTERED

CRF Processing Date: 3/13/2002
Edited by: _____ AZ
Verified by: _____ AZ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☑ Other: Corrected spelling of "Proteases" in 1/207 response _____

*Examiner: Th abov corrections must be communicated to the applicant in th first Office
Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A TIME: 16:47:06

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\03132002\I652743A.raw

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       3 <110> APPLICANT: Norregaard-Madsen, Mads
       4        Ostergaard, Peter Rahbek
       5        Christensen, Claus Bo Voge
       6        Lassen, Soren Flensted
       8 <120> TITLE OF INVENTION: Novel Proteases And Variants Thereof
      10 <130> FILE REFERENCE: 5665.400-US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/652,743A
C--> 12 <141> CURRENT FILING DATE: 2000-08-31
      12 <160> NUMBER OF SEQ ID NOS: 45
      14 <170> SOFTWARE: PatentIn version 3.1
      16 <210> SEQ ID NO: 1
      17 <211> LENGTH: 948
      18 <212> TYPE: DNA
      19 <213> ORGANISM: Bacillus
      21 <220> FEATURE:
      22 <221> NAME/KEY: CDS
      23 <222> LOCATION: (1)..(948)
      24 <223> OTHER INFORMATION:
      27 <220> FEATURE:
      28 <221> NAME/KEY: mat_peptide
      29 <222> LOCATION: (283)..()
      30 <223> OTHER INFORMATION:
      33 <220> FEATURE:
      34 <221> NAME/KEY: sig_peptide
      35 <222> LOCATION: (1)..(93)
      36 <223> OTHER INFORMATION:
      39 <220> FEATURE:
W--> 40 <221> NAME/KEY: pro-peptide
      41 <222> LOCATION: (94)..(282)
      42 <223> OTHER INFORMATION:
      45 <400> SEQUENCE: 1
      46 ttg gtt agt aaa aag agt gtt aaa cga ggt ttg atc aca ggt ctc att        48
      47 Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile
      48                 -90             -85             -80
      50 ggt att tct att tat tct tta ggt atg cac ccg gcc caa gcc gcg cca        96
      51 Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro
      52                 -75             -70             -65
      54 tcg cct cat act cct gtt tca agc gat cct tca tac aaa gcg gaa aca       144
      55 Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
      56         -60             -55             -50
      58 tcg gtt act tat gac cca cac att aag agc gat caa tac ggc ttg tat       192
      59 Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
      60     -45             -40             -35
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RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:47:06

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\03132002\I652743A.raw

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62 tca aaa gcg ttt aca ggc acc ggc aaa gtg aat gaa aca aag gaa aaa        240
63 Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys
64 -30                 -25                 -20                 -15
66 gcg gaa aaa aag tca ccc gcc aaa gct cct tac agc att aaa tcg gtg        288
67 Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val
68                 -10                 -5                  -1 1
70 att ggt tct gat gat cgg aca agg gtc acc aac aca acc gca tat ccg        336
71 Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro
72         5                   10                  15
74 tac aga gcg atc gtt cat att tca agc agc atc ggt tca tgc acc gga        384
75 Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
76         20                  25                  30
78 tgg atg atc ggt ccg aaa acc gtc gca aca gcc gga cac tgc atc tat        432
79 Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
80 35                  40                  45                  50
82 gac aca tca agc ggt tca ttt gcc ggt aca gcc act gtt tcg ccg gga        480
83 Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
84                 55                  60                  65
86 cgg aac ggg aca agc tat cct tac ggc tca gtt aaa tcg acg cgc tac        528
87 Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
88                 70                  75                  80
90 ttt att ccg tca gga tgg aga agc gga aac acc aat tac gat tac gga        576
91 Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
92         85                  90                  95
94 gca atc gaa cta agc gaa ccg atc ggc aat act gtc gga tac ttc gga        624
95 Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
96         100                 105                 110
98 tac tcg tac act act tca tca ctt gtt ggg aca act gtt acc atc agc        672
99 Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
100 115                 120                 125                 130
102 ggc tac cca ggc gat aaa aca gca ggc aca caa tgg cag cat tca gga      720
103 Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
104                 135                 140                 145
106 ccg att gcc atc tcc gaa acg tat aaa ttg cag tac gca atg gac acg      768
107 Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
108                 150                 155                 160
110 tac gga gga caa agc ggt tca ccg gta ttc gaa caa agc agc tcc aga      816
111 Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
112         165                 170                 175
114 acg aac tgt agc ggt ccg tgc tcg ctt gcc gta cac aca aat gga gta      864
115 Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
116     180                 185                 190
118 tac ggc ggc tcc tcg tac aac aga ggc acc cgg att aca aaa gag gtg      912
119 Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val
120 195                 200                 205                 210
122 ttc gac aat ttg acc aac tgg aaa aac agc gca caa                      948
123 Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
124                 215                 220
127 <210> SEQ ID NO: 2
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128 <211> LENGTH: 316
129 <212> TYPE: PRT
130 <213> ORGANISM: Bacillus
132 <400> SEQUENCE: 2
134 Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile
135               -90                 -85                 -80
138 Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro
139           -75                 -70                 -65
142 Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
143           -60                 -55                 -50
146 Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
147       -45                 -40                 -35
150 Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys
151 -30                 -25                 -20                 -15
154 Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val
155               -10                 -5                  -1  1
158 Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro
159           5                   10                  15
162 Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
163       20                  25                  30
166 Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
167 35                  40                  45                  50
170 Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
171               55                  60                  65
174 Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
175           70                  75                  80
178 Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
179           85                  90                  95
182 Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
183       100                 105                 110
186 Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
187 115                 120                 125                 130
190 Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
191               135                 140                 145
194 Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
195           150                 155                 160
198 Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
199           165                 170                 175
202 Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
203       180                 185                 190
206 Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val
207 195                 200                 205                 210
210 Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
211               215                 220
214 <210> SEQ ID NO: 3
215 <211> LENGTH: 1026
216 <212> TYPE: DNA
217 <213> ORGANISM: Bacillus
219 <220> FEATURE:
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RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:47:06

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\03132002\I652743A.raw**

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221 <222> LOCATION: (1)..(1026)
222 <223> OTHER INFORMATION:
225 <220> FEATURE:
226 <221> NAME/KEY: mat_peptide
227 <222> LOCATION: (361)..()
228 <223> OTHER INFORMATION:
231 <220> FEATURE:
232 <221> NAME/KEY: sig_peptide
233 <222> LOCATION: (1)..(78)
234 <223> OTHER INFORMATION:
237 <220> FEATURE:
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W--> `238 <221> NAME/KEY: pro-peptide`
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239 <222> LOCATION: (79)..(360)
240 <223> OTHER INFORMATION:
243 <400> SEQUENCE: 3
244 atg  aaa cta cta tta aaa  ctt act ttt gta tgc  ata ttt atg tta        45
245 Met  Lys Leu Leu Leu Lys  Leu Thr Phe Val Cys  Ile Phe Met Leu
246 -120              -115                -110
248 agt  ggg att cta tcc cca  gta aac gca act caa gct gag act ctt act     93
249 Ser  Gly Ile Leu Ser Pro  Val Asn Ala Thr Gln Ala Glu Thr Leu Thr
250 -105              -100               -95                 -90
252 aaa tta aat aaa ata agt cag aag cag gaa cca tca tat aaa cta gat      141
253 Lys Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp
254                  -85              -80              -75
256 gaa gaa atg gat tat gtt cta att gat ttg gaa aca caa tct gaa tcg      189
257 Glu Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser
258              -70              -65              -60
260 att att tcg ata gga gat aat acc gat ttg gga gat caa tcg ttt act      237
261 Ile Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr
262          -55              -50              -45
264 tct tta ggg aag gtg gga cat gga gaa ctt gag aaa att aac tta gaa      285
265 Ser Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu
266      -40              -35              -30
268 gaa ttt cgt aat cct aat tta aca gta gta gac ccg tta aca cgt aag      333
269 Glu Phe Arg Asn Pro Asn Leu Thr Val Val Asp Pro Leu Thr Arg Lys
270 -25              -20              -15              -10
272 cct att gaa caa aaa atc agc cct ttt gtt gtt ata ggc gat gat ggg      381
273 Pro Ile Glu Gln Lys Ile Ser Pro Phe Val Val Ile Gly Asp Asp Gly
274                  -5              -1 1              5
276 aga aga caa gtt caa aat act tct ttc atg cca ttt cgt gca ctt act      429
277 Arg Arg Gln Val Gln Asn Thr Ser Phe Met Pro Phe Arg Ala Leu Thr
278          10              15              20
280 tat att gag ttt gga aac ctt aca agt aca tgg agt tgt tct gga ggt      477
281 Tyr Ile Glu Phe Gly Asn Leu Thr Ser Thr Trp Ser Cys Ser Gly Gly
282      25              30              35
284 gtg att gga aca gat tta gtt gtt act aat gca cat tgt gta gaa ggt      525
285 Val Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly
286 40              45              50              55
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RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:47:06

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\03132002\I652743A.raw


```
288 tct gtg tta gca ggt act gta gtt cct ggt atg aac aat agt cag tgg      573
289 Ser Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp
290             60              65                  70
292 gca tat ggg cat tat agg gtt act cag att atc tac cct gat caa tac      621
293 Ala Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr
294             75              80                  85
296 aga aat aac ggt gct tca gag ttt gat tat gct ata ctt aga gta gca      669
297 Arg Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala
298             90              95                  100
300 cct gac tct gat gga cgt cat att gga aac aga gct gga att tta tct      717
301 Pro Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser
302     105             110                 115
304 ttt aca gaa aca gga act gtt aac gaa aat act ttt cta aga acg tat      765
305 Phe Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr
306 120             125                 130                 135
308 gga tac ccc ggt gat aaa ata tca gag aca aaa tta att tct ttg tgg      813
309 Gly Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp
310             140                 145                 150
312 gga atg gtt ggt cga tct gat gca ttt ttg cat cga gac cta ctg ttc      861
313 Gly Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe
314             155                 160                 165
316 tac aat atg gac acc tat ttt ggt caa tca ggt tct cct gta tta aac      909
317 Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn
318             170                 175                 180
320 agc gta gat tca atg gtt gcg gtt cat aat gca ggg tat atc gtt ggt      957
321 Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly
322     185                 190                 195
324 ggt aat agg gaa att aat ggt ggt cct aaa atc aga aga gat ttt aca      1005
325 Gly Asn Arg Glu Ile Asn Gly Gly Pro Lys Ile Arg Arg Asp Phe Thr
326 200                 205                 210                 215
328 aac tta ttt aat caa atg aac                                          1026
329 Asn Leu Phe Asn Gln Met Asn
330                 220
333 <210> SEQ ID NO: 4
334 <211> LENGTH: 342
335 <212> TYPE: PRT
336 <213> ORGANISM: Bacillus
338 <400> SEQUENCE: 4
340 Met  Lys Leu Leu Leu Lys  Leu Thr Phe Val Cys  Ile Phe Met Leu
341 -120                -115                -110
344 Ser  Gly Ile Leu Ser Pro  Val Asn Ala Thr Gln Ala Glu Thr Leu Thr
345 -105                -100                -95                 -90
348 Lys Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp
349                 -85                 -80                 -75
352 Glu Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser
353                 -70                 -65                 -60
356 Ile Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr
357         -55                 -50                 -45
360 Ser Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:47:07

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\03132002\I652743A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; N Pos. 21,36
Seq#:20; N Pos. 12,15,18,21,24
Seq#:21; Xaa Pos. 2
Seq#:22; N Pos. 22,25,31
Seq#:23; Xaa Pos. 5
Seq#:24; N Pos. 15,18
Seq#:25; Xaa Pos. 6
Seq#:38; N Pos. 18,21,27
Seq#:39; Xaa Pos. 2,4
Seq#:40; N Pos. 12,15,21
Seq#:44; N Pos. 14,15

W. Moore

1600

RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:16:04

Input Set : **A:\sequence.ST25.txt**
Output Set: N:\CRF3\03132002\I652743A.raw

P.S.

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    3  <110>  APPLICANT: Norregaard-Madsen, Mads
    4         Ostergaard, Peter Rahbek
    5         Christensen, Claus Bo Voge
    6         Lassen, Soren Flensted
    8  <120>  TITLE OF INVENTION: Novel Proteases And Variants Thereof
   10  <130>  FILE REFERENCE: 5665.400-US
C-->12  <140>  CURRENT APPLICATION NUMBER: US/09/652,743A
C-->12  <141>  CURRENT FILING DATE: 2000-08-31
   12  <160>  NUMBER OF SEQ ID NOS: 45
   14  <170>  SOFTWARE: PatentIn version 3.1
   16  <210>  SEQ ID NO: 1
   17  <211>  LENGTH: 948
   18  <212>  TYPE: DNA
   19  <213>  ORGANISM: Bacillus
   21  <220>  FEATURE:
   22  <221>  NAME/KEY: CDS
   23  <222>  LOCATION: (1)..(948)
   24  <223>  OTHER INFORMATION:
   27  <220>  FEATURE:
   28  <221>  NAME/KEY: mat_peptide
   29  <222>  LOCATION: (283)..()
   30  <223>  OTHER INFORMATION:
   33  <220>  FEATURE:
   34  <221>  NAME/KEY: sig_peptide
   35  <222>  LOCATION: (1)..(93)
   36  <223>  OTHER INFORMATION:
   39  <220>  FEATURE:
W-->40  <221>  NAME/KEY: pro-peptide
   41  <222>  LOCATION: (94)..(282)
   42  <223>  OTHER INFORMATION:
   45  <400>  SEQUENCE: 1
   46  ttg gtt agt aaa aag agt gtt aaa cga ggt ttg atc aca ggt ctc att      48
   47  Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile
   48              -90                 -85                 -80
   50  ggt att tct att tat tct tta ggt atg cac ccg gcc caa gcc gcg cca      96
   51  Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro
   52              -75                 -70                 -65
   54  tcg cct cat act cct gtt tca agc gat cct tca tac aaa gcg gaa aca     144
   55  Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
   56              -60                 -55                 -50
   58  tcg gtt act tat gac cca cac att aag agc gat caa tac ggc ttg tat     192
   59  Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
   60          -45                 -40                 -35
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RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:16:04

Input Set : A:\sequence.ST25.txt
Output Set: N:\CRF3\03132002\I652743A.raw

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 62 tca aaa gcg ttt aca ggc acc ggc aaa gtg aat gaa aca aag gaa aaa       240
 63 Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys
 64 -30                 -25                 -20                 -15
 66 gcg gaa aaa aag tca ccc gcc aaa gct cct tac agc att aaa tcg gtg       288
 67 Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val
 68                 -10                  -5                 -1  1
 70 att ggt tct gat gat cgg aca agg gtc acc aac aca acc gca tat ccg       336
 71 Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro
 72          5                  10                  15
 74 tac aga gcg atc gtt cat att tca agc agc atc ggt tca tgc acc gga       384
 75 Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
 76      20                  25                  30
 78 tgg atg atc ggt ccg aaa acc gtc gca aca gcc gga cac tgc atc tat       432
 79 Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
 80 35                  40                  45                  50
 82 gac aca tca agc ggt tca ttt gcc ggt aca gcc act gtt tcg ccg gga       480
 83 Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
 84                  55                  60                  65
 86 cgg aac ggg aca agc tat cct tac ggc tca gtt aaa tcg acg cgc tac       528
 87 Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
 88                  70                  75                  80
 90 ttt att ccg tca gga tgg aga agc gga aac acc aat tac gat tac gga       576
 91 Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
 92          85                  90                  95
 94 gca atc gaa cta agc gaa ccg atc ggc aat act gtc gga tac ttc gga       624
 95 Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
 96      100                 105                 110
 98 tac tcg tac act act tca tca ctt gtt ggg aca act gtt acc atc agc       672
 99 Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
100 115                 120                 125                 130
102 ggc tac cca ggc gat aaa aca gca ggc aca caa tgg cag cat tca gga       720
103 Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
104                 135                 140                 145
106 ccg att gcc atc tcc gaa acg tat aaa ttg cag tac gca atg gac acg       768
107 Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
108                 150                 155                 160
110 tac gga gga caa agc ggt tca ccg gta ttc gaa caa agc agc tcc aga       816
111 Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
112                 165                 170                 175
114 acg aac tgt agc ggt ccg tgc tcg ctt gcc gta cac aca aat gga gta       864
115 Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
116      180                 185                 190
118 tac ggc ggc tcc tcg tac aac aga ggc acc cgg att aca aaa gag gtg       912
119 Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val
120 195                 200                 205                 210
122 ttc gac aat ttg acc aac tgg aaa aac agc gca caa                       948
123 Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
124                 215                 220
127 <210> SEQ ID NO: 2
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128 <211> LENGTH: 316
129 <212> TYPE: PRT
130 <213> ORGANISM: Bacillus
132 <400> SEQUENCE: 2
134 Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile
135               -90               -85               -80
138 Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro
139               -75               -70               -65
142 Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
143               -60               -55               -50
146 Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
147       -45               -40               -35
150 Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys
151 -30               -25               -20               -15
154 Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val
155               -10               -5                -1 1
158 Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro
159       5                 10                15
162 Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
163       20                25                30
166 Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
167 35                40                45                50
170 Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
171               55                60                65
174 Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
175               70                75                80
178 Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
179       85                90                95
182 Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
183       100               105               110
186 Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
187 115               120               125               130
190 Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
191               135               140               145
194 Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
195               150               155               160
198 Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
199       165               170               175
202 Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
203       180               185               190
206 Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val
207 195               200               205               210
210 Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
211               215               220
214 <210> SEQ ID NO: 3
215 <211> LENGTH: 1026
216 <212> TYPE: DNA
217 <213> ORGANISM: Bacillus
219 <220> FEATURE:
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RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:16:04

Input Set : A:\sequence.ST25.txt
Output Set: N:\CRF3\03132002\I652743A.raw

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220 <221> NAME/KEY: CDS
221 <222> LOCATION: (1)..(1026)
222 <223> OTHER INFORMATION:
225 <220> FEATURE:
226 <221> NAME/KEY: mat_peptide
227 <222> LOCATION: (361)..()
228 <223> OTHER INFORMATION:
231 <220> FEATURE:
232 <221> NAME/KEY: sig_peptide
233 <222> LOCATION: (1)..(78)
234 <223> OTHER INFORMATION:
237 <220> FEATURE:
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W--> **238 <221> NAME/KEY: pro-peptide**

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239 <222> LOCATION: (79)..(360)
240 <223> OTHER INFORMATION:
243 <400> SEQUENCE: 3
244 atg aaa cta cta tta aaa  ctt act ttt gta tgc  ata ttt atg tta       45
245 Met Lys Leu Leu Leu Lys  Leu Thr Phe Val Cys  Ile Phe Met Leu
246 -120                -115                 -110
248 agt ggg att cta tcc cca  gta aac gca act caa  gct gag act ctt act   93
249 Ser Gly Ile Leu Ser Pro  Val Asn Ala Thr Gln  Ala Glu Thr Leu Thr
250 -105                -100                 -95                 -90
252 aaa tta aat aaa ata agt cag aag cag gaa cca tca tat aaa cta gat    141
253 Lys Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp
254                -85                 -80                 -75
256 gaa gaa atg gat tat gtt cta att gat ttg gaa aca caa tct gaa tcg    189
257 Glu Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser
258                -70                 -65                 -60
260 att att tcg ata gga gat aat acc gat ttg gga gat caa tcg ttt act    237
261 Ile Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr
262           -55                 -50                 -45
264 tct tta ggg aag gtg gga cat gga gaa ctt gag aaa att aac tta gaa    285
265 Ser Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu
266      -40                 -35                 -30
268 gaa ttt cgt aat cct aat tta aca gta gta gac ccg tta aca cgt aag    333
269 Glu Phe Arg Asn Pro Asn Leu Thr Val Val Asp Pro Leu Thr Arg Lys
270 -25                 -20                 -15                 -10
272 cct att gaa caa aaa atc agc cct ttt gtt gtt ata ggc gat gat ggg    381
273 Pro Ile Glu Gln Lys Ile Ser Pro Phe Val Val Ile Gly Asp Asp Gly
274           -5                  -1 1                  5
276 aga aga caa gtt caa aat act tct ttc atg cca ttt cgt gca ctt act    429
277 Arg Arg Gln Val Gln Asn Thr Ser Phe Met Pro Phe Arg Ala Leu Thr
278           10                  15                  20
280 tat att gag ttt gga aac ctt aca agt aca tgg agt tgt tct gga ggt    477
281 Tyr Ile Glu Phe Gly Asn Leu Thr Ser Thr Trp Ser Cys Ser Gly Gly
282      25                  30                  35
284 gtg att gga aca gat tta gtt gtt act aat gca cat tgt gta gaa ggt    525
285 Val Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly
286 40                  45                  50                  55
```

RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/09/652,743A   TIME: 16:16:04

Input Set : A:\sequence.ST25.txt
Output Set: N:\CRF3\03132002\I652743A.raw

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288 tct gtg tta gca ggt act gta gtt cct ggt atg aac aat agt cag tgg      573
289 Ser Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp
290             60              65              70
292 gca tat ggg cat tat agg gtt act cag att atc tac cct gat caa tac      621
293 Ala Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr
294             75              80              85
296 aga aat aac ggt gct tca gag ttt gat tat gct ata ctt aga gta gca      669
297 Arg Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala
298             90              95              100
300 cct gac tct gat gga cgt cat att gga aac aga gct gga att tta tct      717
301 Pro Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser
302       105             110             115
304 ttt aca gaa aca gga act gtt aac gaa aat act ttt cta aga acg tat      765
305 Phe Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr
306 120             125             130             135
308 gga tac ccc ggt gat aaa ata tca gag aca aaa tta att tct ttg tgg      813
309 Gly Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp
310             140             145             150
312 gga atg gtt ggt cga tct gat gca ttt ttg cat cga gac cta ctg ttc      861
313 Gly Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe
314             155             160             165
316 tac aat atg gac acc tat ttt ggt caa tca ggt tct cct gta tta aac      909
317 Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn
318             170             175             180
320 agc gta gat tca atg gtt gcg gtt cat aat gca ggg tat atc gtt ggt      957
321 Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly
322       185             190             195
324 ggt aat agg gaa att aat ggt ggt cct aaa atc aga aga gat ttt aca     1005
325 Gly Asn Arg Glu Ile Asn Gly Gly Pro Lys Ile Arg Arg Asp Phe Thr
326 200             205             210             215
328 aac tta ttt aat caa atg aac                                        1026
329 Asn Leu Phe Asn Gln Met Asn
330             220
333 <210> SEQ ID NO: 4
334 <211> LENGTH: 342
335 <212> TYPE: PRT
336 <213> ORGANISM: Bacillus
338 <400> SEQUENCE: 4
340 Met  Lys Leu Leu Leu Lys  Leu Thr Phe Val Cys  Ile Phe Met Leu
341 -120                -115                -110
344 Ser  Gly Ile Leu Ser Pro  Val Asn Ala Thr Gln Ala Glu Thr Leu Thr
345 -105                -100                -95                 -90
348 Lys Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp
349             -85                 -80                 -75
352 Glu Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser
353             -70                 -65                 -60
356 Ile Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr
357             -55                 -50                 -45
360 Ser Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu
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VERIFICATION SUMMARY   DATE: 03/13/2002
PATENT APPLICATION: **US/09/652,743A**   TIME: 16:16:05

Input Set : **A:\sequence.ST25.txt**
Output Set: **N:\CRF3\03132002\I652743A.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:40 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:238 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:452 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:650 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:840 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:1038 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:1222 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:1459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1628 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1872 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1903 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44